



## Abstract

The model bacterium, *Desulfovibrio vulgaris* Hildenborough, for which the genome sequence has been fully determined, is being examined for its responses to a variety of stresses that may be expected to be encountered in natural/contaminated settings. We have examined the preliminary transcriptional data from ten treatments to learn whether there are general responses or common themes for responses to stresses by *D. vulgaris*. This anaerobe apparently does not have an ortholog encoding RpoS implicated in the universal stress response in  $\gamma$ -Proteobacteria. Interestingly genes predicted to be controlled by the global regulator Fur appear to be among the most frequently responsive in the genome. The transcriptional responses to increased concentrations of sodium and potassium overlapped strongly, as would be predicted. Curiously, it was not predicted that these salt responses would be shared by the response to reduced temperature. Also counter to our prediction, the response to nitrate was not a simple sum of the responses to sodium and nitrite. Further insights into general patterns of transcription during stresses will be discussed.

## Stresses

Table 1. Stressors examined for transcriptional responses in *D. vulgaris* Hildenborough

Stressor	Concentration or Condition	Time (min)	Comparison culture
Cold	8 C	240	30 C, 240 min
Heat	50 C	15	37 C, 15 min
Oxygen	0.1 %	240	No O <sub>2</sub> , 240 min
Alkaline pH	pH 10	120	pH 7, 0 min
Acid pH	pH 5.5	240	pH 7, 0 min
Nitrite	2.5 mM	60	No NO <sub>2</sub> <sup>-</sup> , 60 min
Nitrate	105 mM	240	No NO <sub>3</sub> <sup>-</sup> , 240 min
Sodium	250 mM	120	No added Na <sup>+</sup> , 120 min
Potassium	250 mM	120	No added K <sup>+</sup> , 120 min
Chromate	0.55 mM	120	No CrO <sub>4</sub> <sup>2-</sup> , 0 min

## Results

Figure 1. Numbers of differentially expressed genes (abs(Z) ≥ 2) for each stress

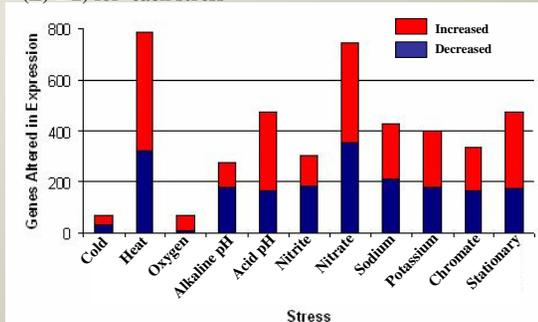


Figure 2. Illustration of the overlap in differentially expressed genes in various stresses

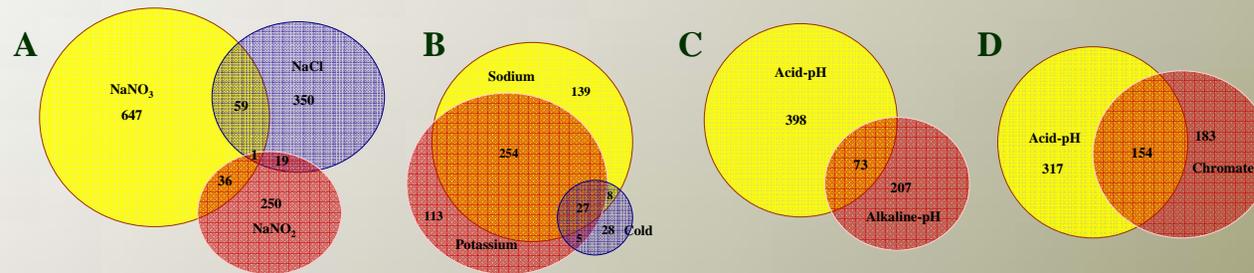
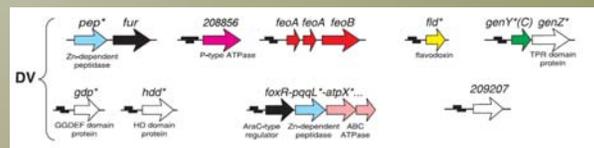


Table 2. *D. vulgaris* Hildenborough transcriptional responses of representative genes in energy metabolism

ORF No.	Gene	Description	SO <sub>4</sub> <sup>2-</sup> Reduction		Stress												
			Cold	Heat	O <sub>2</sub>	pH10	pH5.5	NO <sub>2</sub> <sup>-</sup>	NO <sub>3</sub> <sup>-</sup>	NaCl	KCl	CrO <sub>4</sub> <sup>2-</sup>					
DVU0053	NA <sup>+</sup>	Sulphate permease, putative	1.38				-1.15										
DVU0279	NA <sup>+</sup>	Sulphate permease family protein		1.09				-1.60		2.28	1.85						
DVU1295	sat	Sulphate adenylyltransferase								1.10							
DVU1566	cysD	PAPS reductase, putative	1.99				1.54			2.98							
DVU1597	sir	Sulphite reductase, assimilatory-type								1.61							
DVU0847	apsA	Adenylyl-sulphate reductase, alpha subunit	-1.71							1.73							
DVU0846	apsB	Adenylyl-sulphate reductase, beta subunit	-2.11							1.21							
DVU0402	dxaA	Disimilatory sulphite reductase A, alpha	-3.28														
DVU0403	dxaB	Disimilatory sulphite reductase B, beta	-2.59														
DVU0404	dxaD	Disimilatory sulphite reductase D	-2.96					1.78									1.81
DVU2776	drcC	Disimilatory sulphite reductase C, gamma															
DVU1286	drrP	Integral membrane protein								-1.64							
DVU1287	drrO	Periplasmic (Tat), binds 2[4Fe-4S]								-2.40							
DVU1288	drrJ	Periplasmic (Sec), trihaem cytochrome c								-2.37							
DVU1289	drrK	Cytoplasmic, binds 2[4Fe-4S]	-1.54							-2.20							
DVU1290	drrM	Inner membrane protein binds 2 haem b								-2.65							
DVU1636	pppC	Inorganic pyrophosphatase, Mn-dependent			-1.14						2.14						

ORF No.	Gene	Description	Fur Regulon		Stresses												
			Cold	Heat	O <sub>2</sub>	pH10	pH5.5	NO <sub>2</sub> <sup>-</sup>	NO <sub>3</sub> <sup>-</sup>	NaCl	KCl	CrO <sub>4</sub> <sup>2-</sup>					
DVU0303	NA	Hypothetical protein	2.86	1.49	2.02	1.35	2.79										2.19
DVU0304	NA	Hypothetical protein					2.77										2.34
DVU0763	gdp	GGDEF domain protein	1.50		1.10						1.74						1.97
DVU2378	foxR	Transcriptional regulator, AraC family	1.38				1.66	1.61									
DVU2571	feoB	Fe <sup>2+</sup> transport protein B	3.41		1.74		2.95			1.54	1.15	1.50					
DVU2572	feoA	Fe <sup>2+</sup> transport protein A	3.28		1.86	1.56	3.25			1.49		2.85					
DVU2573	NA	Hypothetical protein	3.77				2.27	2.49		1.25		2.60					
DVU2574	feoA	Fe <sup>2+</sup> transporter component, feoA	3.54				1.40	2.49		1.18		1.97					
DVU2680	fld	Flavodoxin, iron-repressed	1.27	1.22						-1.59							1.74
DVU3330	NA	Fe-regulated P-type ATPase, hypothetical	1.93				1.12	2.09									



D.A. Rodionov, I. Dubchak, A. Arkin, E. Alm, M.S. Gelfand. Reconstruction of regulatory and metabolic pathways in metal-reducing delta-proteobacteria. *Genome Biology* 2004. 5:R90

## Observations

- D. vulgaris* Hildenborough does not encode nitrate reductase. The transcriptional response to nitrate is unexplained and not a simple combination of the response to sodium and that to nitrite.
- The responses to high concentrations of NaCl or KCl have many transcript changes in common. A remarkable number of the genes altered in expression by mildly cold temperature overlapped the salt responses.
- Few transcriptional responses are shared by opposite pH stresses.
- An unexpected number of the same genes were differentially expressed in acid and chromate treatments.
- Genes encoding enzymes for sulfate reduction are not generally upregulated during stress treatments, with the exception of nitrate.
- Genes of the predicted *fur* regulon respond to most stress treatments. A classical "general stress response" has not been identified.
- In the absence of an apparent *rpoS*, a general stress sigma factor, responses to stresses in *D. vulgaris* occur through unidentified signaling pathways.

## Acknowledgements

This work was part of the Virtual Institute for Microbial Stress and Survival (<http://VIMSS.lbl.gov/>) supported by the U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research, and Genomics Program:GTL through contract DE-AC02-05-CH11231 between Lawrence Berkeley National Laboratory and the U.S. Department of Energy